

SEQUENCE LISTING

<110> MURDIN, ANDREW D.
OOMEN, RAYMOND P.
WANG, JOE
DUNN, PAMELA

<120> CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
USES THEREOF

<130> 032931/0230

<140> 09/564,479

<141> 2000-05-03

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<151> 1999-05-03

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<170> PatentIn Ver. 2.1

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Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala
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Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	Lys	Asp	Leu	Lys	Asn	
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Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	195	200	205	
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acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	144
Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	
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Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
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Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr	
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Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	Glu	Thr	Lys	Asn	85	90	95
Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	Leu	Ala	Lys	Tyr	100	105	110
Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	Lys	Leu	Thr	Ser	115	120	125
Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	Ala	Asn	Asn	Asn	130	135	140
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Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	Glu	Asn	Pro	Asp	305	310	315
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				Met Val Asn Pro Ile		
				1 5		
ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt	163					
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu						
	10		15		20	
tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct	211					
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala			30		35	
	25					
caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat	259					
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp			45		50	
	40					
tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg	307					
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met			60		65	
	55					
agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct	355					
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser			75		80	85
	70					
act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg	403					
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr			90		95	100
cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct	451					
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala			105		110	115
tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct	499					
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala			120		125	130
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct	547					
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala			135		140	145
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc	595					
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala			150		155	160
						165
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct	643					
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala			170		175	180
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc	691					
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe			185		190	195
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739					
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys			200		205	210

gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	
caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345 350 355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360 365 370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375 380 385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390 395 400 405	
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410 415 420	
tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
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1456

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<210> 6
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<212> PRT
<213> Chlamydia pneumoniae.
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20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
180 185 190

Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
 260 265 270
 Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
 275 280 285
 Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
 290 295 300
 Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
 305 310 315 320
 Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
 325 330 335
 Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
 340 345 350
 Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
 355 360 365
 Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
 370 375 380
 Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
 385 390 395 400
 Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
 405 410 415
 Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
 420 425 430
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 Ser Ala Gly Val
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<220>
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 acagaaaaag ctgctacaaa cgctatgaaa tacaataact gtgtttggca gtggctcgtc 180
 ggaaagcata gtcaggttcc ttggatcaat ggacagaaaa agcctctata tctttatgga 240

gctttcttaa	tgaacccctt	agcaaaggct	acgaagacta	cgttaaatgg	aaaagaaaac	300
ctagcttggt	ttattggagg	aacttttagg	ggactcagaa	aagctggaga	ctggctctgcc	360
acagtacgtt	atgagtatgt	cgaagccttg	toggttccag	aaatagatgt	ttcagggatt	420
ggccgtggta	atttattaaa	gttttggttc	gcccagcaa	ttgctgctaa	ctatgatcct	480
aaagaggcta	atggttttac	aaattataaa	ggattttccg	ctctatatat	gtatggcatc	540
acagattctc	tatcattcag	agcttatggg	gcttactcca	aaccagcaaa	cgataaactc	600
ggcagtgatt	ttactttccg	aaagtttgat	ctaggtataa	tttcagcgtt	ttaagtcaaa	660
ttttaataaa	atctttaaaa	acaggctcgc	attaattatt	agtgagagct	ttttttttat	720
tttttataat	aaaactaaaa	gattttttatt	attttttgag	ttttt	atg gtt aat cct	777
					Met Val Asn Pro	
					1	
att ggt cca ggt cct	ata gac gaa aca gaa cgc	aca cct ccc gca gat	825			
Ile Gly Pro Gly Pro	Ile Asp Glu Thr Glu Arg Thr	Pro Pro Ala Asp				
5	10	15 20				
ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa	873					
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu						
25 30 35						
gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc	921					
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr						
40 45 50						
gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc	969					
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu						
55 60 65						
atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct	1017					
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser						
70 75 80						
tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct	1065					
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro						
85 90 95 100						
acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	1113					
Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr						
105 110 115						
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct	1161					
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala						
120 125 130						
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg	1209					
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala						
135 140 145						

gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat	1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat	1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	
165 170 175 180	
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc	1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac	1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca	1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct	1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	
230 235 240	
aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
245 250 255 260	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
265 270 275	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
280 285 290	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
295 300 305	
ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa	1737
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys	
310 315 320	
aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca	1785
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr	
325 330 335 340	
gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt	1833
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val	
345 350 355	
tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg	1881
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met	
360 365 370	

tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat	1929
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp	
375 380 385	
tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa	1977
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys	
390 395 400	
gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa	2025
Ala Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala Asp Ala Gln Lys	
405 410 415 420	
gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc	2073
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu	
425 430 435	
aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta	2121
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val	
440 445 450	
ctc ccg ctg cag caa gtt cta tgg atc cga gct cgg tac caa gct tac	2169
Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr	
455 460 465	
gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac	2217
Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp	
470 475 480	
cat cat cat cat cat cat tga	2238
His His His His His His	
485 490	

<210> 8
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 <212> PRT
 <213> Chlamydia pneumoniae

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 35 40 45
 Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
 50 55 60
 Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
 65 70 75 80
 Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
 85 90 95

Ala Thr	Ala Pro	Thr Pro	Pro Pro	Pro Pro	Pro Thr	Phe Asp	Asp Asp	Tyr Lys	Thr	
	100				105			110		
Gln Ala	Gln Thr	Ala Tyr	Asp Thr	Ile Phe	Thr Ser	Thr Ser	Leu Ala			
	115			120			125			
Asp Ile	Gln Ala	Ala Leu	Val Ser	Leu Gln	Asp Ala	Val Thr	Asn Ile			
	130		135		140					
Lys Asp	Thr Ala	Ala Thr	Asp Glu	Glu Thr	Ala Ile	Ala Ala	Glu Trp			
	145		150		155		160			
Glu Thr	Lys Asn	Ala Asp	Ala Val	Lys Val	Gly Ala	Gln Ile	Thr Glu			
		165		170			175			
Leu Ala	Lys Tyr	Ala Ser	Asp Asn	Gln Ala	Ile Leu	Asp Ser	Leu Gly			
	180			185			190			
Lys Leu	Thr Ser	Phe Asp	Leu Leu	Gln Ala	Ala Leu	Leu Gln	Ser Val			
	195		200			205				
Ala Asn	Asn Asn	Lys Ala	Ala Glu	Leu Leu	Lys Glu	Met Gln	Asp Asn			
	210		215		220					
Pro Val	Val Pro	Gly Lys	Thr Pro	Ala Ile	Ala Gln	Ser Leu	Val Asp			
	225		230		235		240			
Gln Thr	Asp Ala	Thr Ala	Thr Gln	Ile Glu	Lys Asp	Gly Asn	Ala Ile			
		245		250			255			
Arg Asp	Ala Tyr	Phe Ala	Gly Gln	Asn Ala	Ser Gly	Ala Val	Glu Asn			
	260			265			270			
Ala Lys	Ser Asn	Asn Ser	Ile Ser	Asn Ile	Asp Ser	Ala Lys	Ala Ala			
	275			280		285				
Ile Ala	Thr Ala	Lys Thr	Gln Ile	Ala Glu	Ala Gln	Lys Lys	Phe Pro			
	290		295		300					
Asp Ser	Pro Ile	Leu Gln	Glu Ala	Glu Gln	Met Val	Ile Gln	Ala Glu			
	305		310		315		320			
Lys Asp	Leu Lys	Asn Ile	Lys Pro	Ala Asp	Gly Ser	Asp Val	Pro Asn			
		325		330			335			
Pro Gly	Thr Thr	Val Gly	Gly Ser	Lys Gln	Gln Gly	Ser Ser	Ile Gly			
		340		345			350			
Ser Ile	Arg Val	Ser Met	Leu Leu	Asp Asp	Ala Glu	Asn Glu	Thr Ala			
	355		360			365				
Ser Ile	Leu Met	Ser Gly	Phe Arg	Gln Met	Ile His	Met Phe	Asn Thr			
	370		375		380					
Glu Asn	Pro Asp	Ser Gln	Ala Ala	Gln Gln	Glu Leu	Ala Ala	Gln Ala			
	385		390		395		400			

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
 405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
 420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
 435 440 445

Ser Ala Gly Val Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg
 450 455 460

Tyr Gln Ala Tyr Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
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Ser Ala Val Asp His His His His His His
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<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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43

<210> 10

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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gcgccggatc ccttggagat aaccagaata tagag

35

<210> 11

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

ataagaatgc ggccgccacc atgagtctgg cagataagct ggg

43

<210> 12

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

gcgccggatc ccttggagat aaccagaata ta

32

<210> 13

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

gctctagacc gccatgacaa aaaaacatta tgcttggg

38

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

cgggatccat agaacttgct gcagcggg

28